

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: OSUMI Chieko  
NOZAKI Jinshi  
KIDA Takao

(ii) TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR PRODUCING RAFFINOSE, AND TRANSGENIC PLANT

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.  
(B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
(C) CITY: ARLINGTON  
(D) STATE: VIRGINIA  
(E) COUNTRY: USA  
(F) ZIP: 22202

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) ATTORNEY/AGENT INFORMATION:  
(A) NAME: NORMAN F. OBLON  
(B) REGISTRATION NUMBER: 24,618

(vii) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (703)-413-3000  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr Leu Thr Val His Pro Gln  
1 5 10 15  
Gly Val Ile Glu Gly Val Arg His Leu Val Asp Gly Gly Cys  
20 25 30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

COPY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ro Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp  
1 5 10 15  
er Arg His

2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Asp Gln Asp Gln Met Val Val Gln Val Pro Trp Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: cucumber (*Cucumis sativas*)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 56..2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAAAACAAAC CCTTCTTTA GTTTTTGGG TTTGTTCTT CTTTCTTCT CACAA ATG 58  
Met  
1  
GCT CCT AGT TTT AAA AAT GGT GGC TCC AAC GTA GTT TCA TTT GAT GGC 106  
Ala Pro Ser Phe Lys Asn Gly Gly Ser Asn Val Val Ser Phe Asp Gly  
5 10 15  
TTA AAT GAC ATG TCG TCA CCG TTT GCA ATC GAC GGA TCG GAT TTC ACT 154  
Leu Asn Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe Thr  
20 25 30  
GTG AAC GGT CAT TCG TTT CTG TCC GAT GTT CCT GAG AAC ATT GTT GCT 202  
Val Asn Gly His Ser Phe Leu Ser Asp Val Pro Glu Asn Ile Val Ala  
35 40 45  
TCT CCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT GGT 250  
Ser Pro Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro Val Ser Val Gly  
50 55 60 65  
TGC TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT AGC CGA CAT GTT GTT 298  
Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser Arg His Val Val  
70 75 80  
TCG ATT GGG AAG CTG AAG GAT ATT CGG TTT ATG AGT ATT TTC AGG TTT 346  
Ser Ile Gly Lys Leu Lys Asp Ile Arg Phe Met Ser Ile Phe Arg Phe

85	90	95	
AG GTT TGG TGG ACT ACA CAC TGG GTT GGT CGA AAT GGT GGG GAT CTT ys Val Trp Trp Thr Thr His Trp Val Gly Arg Asn Gly Gly Asp Leu			394
100	105	110	
GAA TCG GAG ACT CAG ATT GTG ATC CTT GAG AAG TCA GAT TCT GGT CGA lu Ser Glu Thr Gln Ile Val Ile Leu Glu Lys Ser Asp Ser Gly Arg			442
115	120	125	
CCG TAT GTT TTC CTT CTT CCG ATC GTT GAG GGA CCG TTC CGA ACC TCG Pro Tyr Val Phe Leu Leu Pro Ile Val Glu Gly Pro Phe Arg Thr Ser			490
130	135	140	145
ATT CAG CCT GGG GAT GAT GAC TTT GTC GAT GTT TGT GTC GAG AGT GGT Ile Gln Pro Gly Asp Asp Asp Phe Val Asp Val Cys Val Glu Ser Gly			538
150	155	160	
TCG TCG AAA GTT GAT GCA TCG TTC CGA AGT ATG TTG TAT CTT CAT Ser Ser Lys Val Val Asp Ala Ser Phe Arg Ser Met Leu Tyr Leu His			586
165	170	175	
GCT GGT GAT GAT CCG TTT GCA CTT GTT AAA GAG GCG ATG AAG ATC GTG Ala Gly Asp Asp Pro Phe Ala Leu Val Lys Glu Ala Met Lys Ile Val			634
180	185	190	
AGG ACC CAT CTT GGA ACT TTT CGC TTG TTG GAG GAG AAG ACT CCA CCA Arg Thr His Leu Gly Thr Phe Arg Leu Leu Glu Glu Lys Thr Pro Pro			682
195	200	205	
GGT ATC GTG GAC AAA TTC GGT TGG TGC ACG TGG GAC GCG TTT TAC CTA Sly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr Leu			730
210	215	220	225
ACG GTT CAT CCA CAG GGC GTA ATA GAA GGC GTG AGG CAT CTC GTC GAC Thr Val His Pro Gln Gly Val Ile Glu Gly Val Arg His Leu Val Asp			778
230	235	240	
GGC GGT TGT CCT CCC GGT TTA GTC CTA ATC GAC GAT GGT TGG CAA TCC Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp Asp Gly Trp Gln Ser			826
245	250	255	
ATC GGA CAC GAT TCG GAT CCC ATC ACC AAA GAA GGA ATG AAC CAA ACC Ile Gly His Asp Ser Asp Pro Ile Thr Lys Glu Gly Met Asn Gln Thr			874
260	265	270	
GTC GCC GGC GAG CAA ATG CCC TGC CGT CTT TTG AAA TTC CAA GAG AAT Val Ala Gly Glu Gln Met Pro Cys Arg Leu Leu Lys Phe Gln Glu Asn			922
275	280	285	
TAC AAA TTC CGT GAC TAC GTC AAT CCC AAG GCC ACC GGC CCC CGA GCC Tyr Lys Phe Arg Asp Tyr Val Asn Pro Lys Ala Thr Gly Pro Arg Ala			970
290	295	300	305
GGC CAG AAG GGG ATG AAG GCG TTT ATA GAT GAA CTC AAA GGA GAG TTT Gly Gln Lys Gly Met Lys Ala Phe Ile Asp Glu Leu Lys Gly Glu Phe			1018
310	315	320	
AAG ACT GTG GAG CAT GTT TAT GTT TGG CAT GCT TTG TGT GGA TAT TGG Lys Thr Val Glu His Val Tyr Val Trp His Ala Leu Cys Gly Tyr Trp			1066
325	330	335	
GGT GGC CTT CGC CCG CAG GTG CCT GGC TTG CCT GAG GCA CGT GTG ATT Gly Gly Leu Arg Pro Gln Val Pro Gly Leu Pro Glu Ala Arg Val Ile			1114
340	345	350	

AG CCA GTG CTT TCA CCA GGG CTG CAG ATG ACG ATG GAG GAT TTG GCG	1162
In Pro Val Leu Ser Pro Gly Leu Gln Met Thr Met Glu Asp Leu Ala	
355 360 365	
TG GAT AAG ATT GTT CTT CAT AAG GTC GGG CTG GTC CCG CCG GAG AAG	1210
al Asp Lys Ile Val Leu His Lys Val Gly Leu Val Pro Pro Glu Lys	
70 375 380 385	
CT GAG GAG ATG TAC GAA GGA CTT CAT GCT CAT TTG GAA AAA GTT GGG	1258
la Glu Glu Met Tyr Glu Gly Leu His Ala His Leu Glu Lys Val Gly	
390 395 400	
TC GAC GGT GTT AAG ATT GAC GTT ATC CAC CTA TTG GAG ATG TTG TGT	1306
le Asp Gly Val Lys Ile Asp Val Ile His Leu Leu Glu Met Leu Cys	
405 410 415	
AA GAC TAT GGA GGG AGA GTG GAT TTG GCA AAG GCA TAT TAC AAA GCA	1354
lu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala Tyr Tyr Lys Ala	
420 425 430	
TG ACC AAA TCA ATA AAT AAA CAT TTT AAA GGA AAT GGA GTC ATT GCA	1402
Iet Thr Lys Ser Ile Asn Lys His Phe Lys Gly Asn Gly Val Ile Ala	
435 440 445	
GT ATG GAA CAT TGT AAC GAC TTC ATG TTC CTT GGC ACG GAA GCT ATC	1450
Ser Met Glu His Cys Asn Asp Phe Met Phe Leu Gly Thr Glu Ala Ile	
50 455 460 465	
CT CTT GGT CGT GTT GGT GAT GAC TTT TGG TGC ACG GAC CCC TCT GGT	1498
Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro Ser Gly	
470 475 480	
GAT CCA AAC GGT ACG TTT TGG CTC CAA GGA TGT CAC ATG GTT CAT TGT	1546
Asp Pro Asn Gly Thr Phe Trp Leu Gln Gly Cys His Met Val His Cys	
485 490 495	
GCC AAC GAC AGC TTG TGG ATG GGG AAC TTC ATC CAC CCT GAC TGG GAT	1594
Ala Asn Asp Ser Leu Trp Met Gly Asn Phe Ile His Pro Asp Trp Asp	
500 505 510	
ATG TTC CAA TCC ACC CAC CCT TGT GCC GCC TTC CAT GCT GCC TCT CGA	1642
Met Phe Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser Arg	
515 520 525	
GCC ATC TCT GGT GGC CCG ATC TAT GTT AGT GAT TCT GTG GGA AAG CAT	1690
Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Lys His	
530 535 540 545	
AAC TTT GAT CTT CTG AAA AAA CTA GTG CTT CCT GAT GGA TCG ATC CTT	1738
Asn Phe Asp Leu Leu Lys Leu Val Leu Pro Asp Gly Ser Ile Leu	
550 555 560	
CGA AGT GAG TAC TAT GCA CTC CCG ACT CGC GAT TGT TTG TTT GAA GAC	1786
Arg Ser Glu Tyr Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu Asp	
565 570 575	
CCT TTG CAT AAT GGA GAA ACT ATG CTT AAG ATT TGG AAT CTC AAC AAG	1834
Pro Leu His Asn Gly Glu Thr Met Leu Lys Ile Trp Asn Leu Asn Lys	
580 585 590	
TTC ACT GGA GTG ATT GGT GCA TTC AAC TGC CAA GGA GGA GGA TGG TGT	1882
Phe Thr Gly Val Ile Gly Ala Phe Asn Cys Gln Gly Gly Gly Trp Cys	
595 600 605	
CGT GAG ACA CGC CGC AAC CAA TGC TTT TCA CAA TAC TCA AAA CGA GTG	1930

sg Glu Thr Arg Arg Asn Gln Cys Phe Ser Gln Tyr Ser Lys Arg Val			
10	615	620	625
CA TCC AAA ACT AAC CCA AAA GAC ATA GAA TGG CAC AGT GGA GAA AAC			1978
hr Ser Lys Thr Asn Pro Lys Asp Ile Glu Trp His Ser Gly Glu Asn			
630	635	640	
CT ATC TCT ATT GAA GGC GTT AAA ACC TTT GCG CTT TAC CTC TAT CAA			2026
ro Ile Ser Ile Glu Gly Val Lys Thr Phe Ala Leu Tyr Leu Tyr Gln			
645	650	655	
CC AAA AAA CTT ATC CTC TCC AAG CCC TCT CAA GAT CTT GAC ATA GCT			2074
la Lys Lys Leu Ile Leu Ser Lys Pro Ser Gln Asp Leu Asp Ile Ala			
660	665	670	
TT GAC CCA TTC GAA TTC GAG CTC ATC ACT GTT TCA CCA GTG ACC AAA			2122
eu Asp Pro Phe Glu Phe Glu Leu Ile Thr Val Ser Pro Val Thr Lys			
675	680	685	
TC ATC CAA ACT TCT CTA CAC TTT GCC CCA ATT GGG CTG GTG AAC ATG			2170
eu Ile Gln Thr Ser Leu His Phe Ala Pro Ile Gly Leu Val Asn Met			
90	695	700	705
TT AAC ACT AGT GGA GCC ATC CAA TCT GTG GAC TAT GAC GAT GAC CTA			2218
eu Asn Thr Ser Gly Ala Ile Gln Ser Val Asp Tyr Asp Asp Asp Leu			
710	715	720	
GC TCA GTC GAG ATT GGT GTC AAA GGG TGT GGT GAG ATG CGA GTA TTT			2266
ter Ser Val Glu Ile Gly Val Lys Gly Cys Gly Glu Met Arg Val Phe			
725	730	735	
CA TCG AAA AAA CCA AGG GCT TGT CGT ATT GAT GGG GAG GAT GTT GGG			2314
ala Ser Lys Lys Pro Arg Ala Cys Arg Ile Asp Gly Glu Asp Val Gly			
740	745	750	
TC AAG TAT GAT CAG GAC CAA ATG GTG GTG GTT CAA GTG CCA TGG CCA			2362
Phe Lys Tyr Asp Gln Asp Gln Met Val Val Val Gln Val Pro Trp Pro			
755	760	765	
ATT GAT TCT TCA TCG GGT GGC ATT TCG GTT ATC GAG TAC TTG TTT			2407
Ile Asp Ser Ser Gly Gly Ile Ser Val Ile Glu Tyr Leu Phe			
770	775	780	
TAATTTTAT TTATGTAAGC TCAATGATTG TTGTTGTTGT CGCTGTTGTT GCTATCAATG			2467
TATTTCTCTC CAAAAGAAAA TTATGTGTAA TTTGGAGAGT AATTAAGTGA			2517

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Pro Ser Phe Lys Asn Gly Gly Ser Asn Val Val Ser Phe Asp			
1	5	10	15
Gly Leu Asn Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe			
20	25	30	
Thr Val Asn Gly His Ser Phe Leu Ser Asp Val Pro Glu Asn Ile Val			
35	40	45	
Ala Ser Pro Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro Val Ser Val			

50

55

60

Gly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser Arg His Val  
 65                    70                    75                    80  
 Val Ser Ile Gly Lys Leu Lys Asp Ile Arg Phe Met Ser Ile Phe Arg  
       85                    90                    95  
 Phe Lys Val Trp Trp Thr Thr His Trp Val Gly Arg Asn Gly Gly Asp  
       100                    105                    110  
 Leu Glu Ser Glu Thr Gln Ile Val Ile Leu Glu Lys Ser Asp Ser Gly  
       115                    120                    125  
 Arg Pro Tyr Val Phe Leu Leu Pro Ile Val Glu Gly Pro Phe Arg Thr  
       130                    135                    140  
 Ser Ile Gln Pro Gly Asp Asp Asp Phe Val Asp Val Cys Val Glu Ser  
       145                    150                    155                    160  
 Gly Ser Ser Lys Val Val Asp Ala Ser Phe Arg Ser Met Leu Tyr Leu  
       165                    170                    175  
 His Ala Gly Asp Asp Pro Phe Ala Leu Val Lys Glu Ala Met Lys Ile  
       180                    185                    190  
 Val Arg Thr His Leu Gly Thr Phe Arg Leu Leu Glu Glu Lys Thr Pro  
       195                    200                    205  
 Pro Gly Ile Val Asp Lys Phe Gly Trp Cys Thr Trp Asp Ala Phe Tyr  
       210                    215                    220  
 Leu Thr Val His Pro Gln Gly Val Ile Glu Gly Val Arg His Leu Val  
       225                    230                    235                    240  
 Asp Gly Gly Cys Pro Pro Gly Leu Val Leu Ile Asp Asp Gly Trp Gln  
       245                    250                    255  
 Ser Ile Gly His Asp Ser Asp Pro Ile Thr Lys Glu Gly Met Asn Gln  
       260                    265                    270  
 Thr Val Ala Gly Glu Gln Met Pro Cys Arg Leu Leu Lys Phe Gln Glu  
       275                    280                    285  
 Asn Tyr Lys Phe Arg Asp Tyr Val Asn Pro Lys Ala Thr Gly Pro Arg  
       290                    295                    300  
 Ala Gly Gln Lys Gly Met Lys Ala Phe Ile Asp Glu Leu Lys Gly Glu  
       305                    310                    315                    320  
 Phe Lys Thr Val Glu His Val Tyr Val Trp His Ala Leu Cys Gly Tyr  
       325                    330                    335  
 Trp Gly Gly Leu Arg Pro Gln Val Pro Gly Leu Pro Glu Ala Arg Val  
       340                    345                    350  
 Ile Gln Pro Val Leu Ser Pro Gly Leu Gln Met Thr Met Glu Asp Leu  
       355                    360                    365  
 Ala Val Asp Lys Ile Val Leu His Lys Val Gly Leu Val Pro Pro Glu  
       370                    375                    380  
 Lys Ala Glu Glu Met Tyr Glu Gly Leu His Ala His Leu Glu Lys Val  
       385                    390                    395                    400  
 Gly Ile Asp Gly Val Lys Ile Asp Val Ile His Leu Leu Glu Met Leu  
       405                    410                    415  
 Cys Glu Asp Tyr Gly Gly Arg Val Asp Leu Ala Lys Ala Tyr Tyr Lys  
       420                    425                    430  
 Ala Met Thr Lys Ser Ile Asn Lys His Phe Lys Gly Asn Gly Val Ile  
       435                    440                    445

la Ser Met Glu His Cys Asn Asp Phe Met Phe Leu Gly Thr Glu Ala  
 450 455 460  
 le Ser Leu Gly Arg Val Gly Asp Asp Phe Trp Cys Thr Asp Pro Ser  
 465 470 475 480  
 lly Asp Pro Asn Gly Thr Phe Trp Leu Gln Gly Cys His Met Val His  
 485 490 495  
 lys Ala Asn Asp Ser Leu Trp Met Gly Asn Phe Ile His Pro Asp Trp  
 500 505 510  
 Asp Met Phe Gln Ser Thr His Pro Cys Ala Ala Phe His Ala Ala Ser  
 515 520 525  
 Arg Ala Ile Ser Gly Gly Pro Ile Tyr Val Ser Asp Ser Val Gly Lys  
 530 535 540  
 His Asn Phe Asp Leu Leu Lys Lys Leu Val Leu Pro Asp Gly Ser Ile  
 545 550 555 560  
 Leu Arg Ser Glu Tyr Tyr Ala Leu Pro Thr Arg Asp Cys Leu Phe Glu  
 565 570 575  
 Asp Pro Leu His Asn Gly Glu Thr Met Leu Lys Ile Trp Asn Leu Asn  
 580 585 590  
 Cys Phe Thr Gly Val Ile Gly Ala Phe Asn Cys Gln Gly Gly Trp  
 595 600 605  
 Cys Arg Glu Thr Arg Arg Asn Gln Cys Phe Ser Gln Tyr Ser Lys Arg  
 610 615 620  
 Val Thr Ser Lys Thr Asn Pro Lys Asp Ile Glu Trp His Ser Gly Glu  
 625 630 635 640  
 Asn Pro Ile Ser Ile Glu Gly Val Lys Thr Phe Ala Leu Tyr Leu Tyr  
 645 650 655  
 Gln Ala Lys Lys Leu Ile Leu Ser Lys Pro Ser Gln Asp Leu Asp Ile  
 660 665 670  
 Ala Leu Asp Pro Phe Glu Phe Glu Leu Ile Thr Val Ser Pro Val Thr  
 675 680 685  
 Lys Leu Ile Gln Thr Ser Leu His Phe Ala Pro Ile Gly Leu Val Asn  
 690 695 700  
 Met Leu Asn Thr Ser Gly Ala Ile Gln Ser Val Asp Tyr Asp Asp Asp  
 705 710 715 720  
 Leu Ser Ser Val Glu Ile Gly Val Lys Gly Cys Gly Glu Met Arg Val  
 725 730 735  
 Phe Ala Ser Lys Lys Pro Arg Ala Cys Arg Ile Asp Gly Glu Asp Val  
 740 745 750  
 Gly Phe Lys Tyr Asp Gln Asp Gln Met Val Val Val Gln Val Pro Trp  
 755 760 765  
 Pro Ile Asp Ser Ser Ser Gly Gly Ile Ser Val Ile Glu Tyr Leu Phe  
 770 775 780

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TYTAYCTBA CHGTNCAYCC TCA

23

2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TYTAYCTBA CHGTNCAYCC CCA

23

2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TYTAYCTBA CHGTNCAYCC ACA

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TYTAYCTBA CHGTNCAYCC GCA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:  
(B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

26

ARGGNGTNM GNCAYCTRGT NGAYGG

2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

26

ARGGNGTNM GNCAYCTYGT NGAYGG

2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

26

3ARGGNGTNM GNCAYTTRGT NGAYGG

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 3 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TNGGNTGYT TYGTNGGYTT YGAYGC

26

2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 3 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TNGGNTGYT TYGTNGGRTT YGAYGC

26

2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 9 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TYGAYGCNT CNGARCCCHGA YTCDCGNCA

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 9 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TYGAYGCNT CNGARCCCHGA YTCDAGYCA

30

2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

:AYCARGAYC TRATGGTNGT

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2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:

- (B) LOCATION:

- (D) OTHER INFORMATION: N at 6 and 15 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCRTCNACYA GRTGNCKNAC NCCYTC

26

2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:

- (B) LOCATION:

- (D) OTHER INFORMATION: N at 6 and 15 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCRTCNACRA GRTGNCKNAC NCCYTC

26

2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"  
(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(D) OTHER INFORMATION: N at 6 and 15 = inosine  
Other N = A, G, C, or T  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

26

CRTCNACYA TRTGNCKNAC NCCYTC

2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"  
(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(D) OTHER INFORMATION: N at 3 and 18 = inosine  
Other N = A, G, C, or T  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

29

'GNCGHGART CDGGYTCNGA NGCRTCAA

2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"  
(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(D) OTHER INFORMATION: N at 19 = inosine  
Other N = A, G, C, or T  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

30

RTGRCTHGAR TCDGGYTCNG ANGCRTCAA